

Development of national genomic evaluations for health traits in U.S. Holsteins

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Summary

The objectives of this research were to develop and implement genetic and genomic evaluations for resistance to six common health events reported in U.S. dairy herds. Events included hypocalcemia (milk fever), displaced abomasum, ketosis, mastitis, metritis, and retained placenta. Dairy Records Management Systems (Raleigh, NC) provided producer-recorded data for these six health events. After applying standardization and editing constraints to the data, there were 3.1 million records from 1.7 million Holsteins. Variance components were estimated for each trait using univariate linear animal models. Heritability estimates on the observed scale were 0.6%, 1.1%, 1.2%, 3.1%, 1.4%, and 1.0% for hypocalcemia, displaced abomasum, ketosis, mastitis, metritis, and retained placenta, respectively. Traditional predicted transmitting abilities (PTA) were calculated for 63.1 million Holsteins through pedigree relationships using a linear animal model including effects of year-season, age-parity, herd-year, and permanent environment, as well as a regression on inbreeding. Genomic PTA were calculated using 60,671 markers for 1.36 million Holsteins. Young animal reliabilities averaged 11-18% in the pedigree-based model versus 40-49% using genomic information. Average reliabilities for proven animals ranged from 20-33% in the pedigree-based model compared to 44-56% from genomic predictions. Health trait PTA were correlated with several traits included in the Net Merit index (NM\$). Estimated cost per case for each health event was estimated using recent calculations of direct costs in literature, while also accounting for adjustments traditionally made for abnormal test-day records. Direct costs for each health event ranged from \$28 for ketosis up to \$197 for displaced abomasum. The six health traits together will receive 2-3% of the total relative emphasis when included in NM\$.

Keywords: dairy, economic, genomic evaluation, health trait

Introduction

Genetic selection of dairy animals for improved resistance to common health events is gaining interest throughout the dairy industry. Animals that experience health events during their lifetime are less profitable due to the costs of veterinary treatments, discarded milk, and additional farm labor (*e.g.*, Liang *et al.*, 2017) and shorter herd life.

U.S. producers have previously benefited from indirect genetic improvement of health through correlations with traits such as somatic cell score, productive life, and livability. Further genetic progress is expected from direct selection of health traits. A limitation to the development of direct genetic measures for health traits in the U.S. has been the lack of a centralized system to collect health data at a national level. Previous research has shown that

selection for resistance to common health events is possible through the use of producer-recorded data (e.g., Parker Gaddis *et al.*, 2014; Vukasinovic *et al.*, 2016; Zwald *et al.*, 2004). The Council on Dairy Cattle Breeding (CDCB) sought to develop and implement a pipeline for national genetic and genomic evaluations for resistance to six common health events. This included estimation of appropriate economic weights for the future inclusion of these traits in NM\$.

Materials and methods

Data

Producer-recorded health data for 6 health events (MFEV = milk fever or hypocalcemia; DA = displaced abomasum; KETO = ketosis; MAST = mastitis; METR = metritis; RETP = retained placenta) from 1991 to 2016 were provided by Dairy Records Management Systems (Raleigh, NC). Producer-reported acronyms were converted to standardized acronyms. Editing constraints were applied by health event similarly to that described in Parker Gaddis *et al.* (2012). After editing, there were 3,131,918 records from 1,721,117 cows representing 2,192 herds across 44 states. Genotypes included the 60,671 SNP utilized in routine U.S. genomic evaluations by CDCB.

Genetic and genomic analyses

Variance components for each health event were estimated from univariate linear animal models implemented with AIREMLF90 version 1.122 (Misztal *et al.*, 2002). Traditional PTA were estimated using a univariate BLUP repeatability animal model, similar to those used for routine U.S. national genetic evaluations (VanRaden *et al.*, 2014). Models included effects of year-season, age-parity, herd-year, and permanent environment, as well as a regression on inbreeding. Approximately 63 million pedigree records were included. Allele substitution effects were estimated from deregressed traditional PTA for the 60,671 SNP included in the December 2016 U.S. genetic evaluation. An infinitesimal alleles model was used with a heavy-tailed prior (VanRaden, 2008). Genomic PTA were calculated for 1.36 million Holsteins by combining direct genomic prediction, parent average computed from the subset of genotyped ancestors using traditional relationships, and parent average in a selection index (VanRaden *et al.*, 2009). PTA correlations were estimated between the health traits and traits in NM\$ including protein yield, productive life, livability, SCS, daughter pregnancy rate, and heifer and cow conception rate. For MFEV and RETP, correlations were calculated using bulls born since 1990 with reliability $\geq 75\%$. For all other traits, correlations were calculated using bulls born since 1990 with reliability $\geq 90\%$.

Economic index

An analysis was conducted to determine if yield losses associated with health conditions are fully accounted for in NM\$. In routine calculations, test day yields that are $< 60\%$ or $> 150\%$ of predicted test day yield are designated as abnormal and adjusted to these limits (Wiggans *et al.*, 2003). Test days coded by the farmer as sick may not be used in the computation of lactation records based on ICAR guidelines on missing results and abnormal intervals (International Committee for Animal Recording, 2016). Milk, fat, and protein lactation yields were analyzed with abnormal and sick TD included at their original values compared to yields with editing and adjustments applied as described by Wiggans *et al.* (2003).

To develop appropriate economic weights, two recent studies were used to estimate direct treatment costs for each health event. Liang *et al.* (2017) estimated direct treatment, labor, and discarded milk costs for health disorders from veterinary and producer surveys. Donnelly *et al.* (2017) collected health treatment costs from eight herds located in Minnesota. The use of direct treatment costs prevented including costs that are already accounted for in NM\$ calculations, such as declines in production, fertility, and longevity.

Results and discussion

The incidence rate for each health event was 1.3% for MFEV, 2.1% for DA, 3.9% for KETO, 10.2% for MAST, 6.2% for METR, and 3.6% for RETP. These incidence rates align with estimates previously reported in literature. Heritability estimates on the observed scale were 0.6% for MFEV, 1.1% for DA, 1.2% for KETO, 3.1% for MAST, 1.4% for METR, and 1.0% for RETP. The heritability estimates correspond well with previous estimates reported in literature using linear models.

Traditional and genomic reliabilities were estimated for young bulls (those with PTA reliability = PA reliability) and proven bulls (those with PTA reliability > PA reliability). Average reliability for each health trait is provided in Table 1. Average gains from genomic analyses were 22.1 points for proven animals and 28.2 points for young animals.

Table 1. Mean traditional and genomic reliability (REL) for young and proven bulls for each health event.

	Proven bulls		Young bulls	
	Traditional REL	Genomic REL	Traditional REL	Genomic REL
Hypocalcemia	20.0	44.2	10.9	40.0
Displaced abomasum	25.7	47.1	14.6	41.8
Ketosis	24.0	46.2	13.4	41.2
Mastitis	33.3	56.3	18.3	49.4
Metritis	27.6	48.1	15.4	42.2
Retained placenta	25.6	46.7	14.2	41.6

Health trait PTA represent an animal's resistance to a health event such that positive values are favorable. Correlations between the health traits and traits already included in NM\$ were as expected (Table 2). Correlations with the yield trait (protein) were not significant for any health trait. The largest correlation with SCS was with MAST. Of the health traits, DA had the highest correlation with livability, indicating that animals experiencing DA are least likely to survive in the herd. Most traits (with the exception of MFEV) were significantly favorably correlated with daughter pregnancy rate and cow conception rate.

Table 2. Estimated correlations between the health traits evaluations and traits¹ already included in Net Merit

	Protein	PL	LIV	SCS	DPR	CCR	HCR
Hypocalcemia	0.18	0.15	0.19	-0.29*	0.003	0.01	0.02
Displaced abomasum	0.23	0.35*	0.47*	-0.13	0.32*	0.28*	0.24

Ketosis	0.03	0.33	0.27	-0.19	0.59*	0.49*	0.07
Mastitis	0.06	0.39*	0.22*	-0.68*	0.20*	0.21*	0.06
Metritis	0.05	0.32*	0.26*	-0.09	0.46*	0.41*	0.23*
Retained placenta	-0.03	0.17*	0.13*	-0.10	0.14*	0.13*	0.12*

¹ PL = productive life; LIV = livability; SCS = somatic cell score; DPR = daughter pregnancy rate; CCR = cow conception rate; HCR = heifer conception rate

* Significant at $P < 0.05$

Investigation of milk, fat, and protein lactation yields with and without adjustment for unhealthy versus healthy cows indicated that most health traits had only 1 kg differences for fat and 0.5 kg difference for protein. The value per lactation is \$1.23 for fat and \$1.32 for protein, giving only about \$4 more value to add to the direct health costs per case to account for unadjusted yield minus the published (adjusted) yield. Only DA had larger differences of 2.7 kg for fat and 4 kg for protein, but those add only \$19 to the \$178 value of direct costs assumed for DA. The larger impact is likely due to the acute effects of DA requiring surgery, thus making such cows more likely to be coded as sick or detected as abnormal on test day.

Inclusion of MAST will cause a reduction of the value assigned to SCS in the NM\$ formula. Previously, the per lactation value of PTA SCS included \$24 for direct premiums and \$20 for indirect MAST costs such as labor, drugs, discarded milk, and milk shipments lost because of antibiotic residue. However, the extra indirect cost of MAST from SCS should be \$3.70 as opposed to the \$20 assumed previously. The 2017 NM\$ formula gives -6.5% emphasis to PTA SCS, but should have given only -4.0% with these assumptions, and will reduce to -3.5% when MAST is included directly.

Average direct costs between the two aforementioned studies were used to provide an estimate of economic cost for each health event. Average cost estimates were \$38 for hypocalcemia, \$178 for displaced abomasum, \$28 for ketosis, \$72 for mastitis (including diagnosis), \$105 for metritis, and \$64 for retained placenta. These values were modified based on the adjusted yield results described above. Table 3 describes the properties and relative values for health traits as well as livability for comparison. Also included in Table 3 is a combined health index that is a weighted estimate incorporating all 6 health traits.

Table 3. Properties and relative values of GPTA for health traits and livability (LIV).

	Min PTA	Max PTA	PTA SD	\$ / case	Relative value (SD × \$) / ∑ all	
					% of health index	% of NM\$
Hypocalcemia	-0.9	+0.6	0.4	38 - 4 = 34	3%	0.07%
Displaced abomasum	-1.8	+1.8	1.0	178 + 19 = 197	39%	0.90%
Ketosis	-2.3	+2.1	0.9	28 + 0 = 28	5%	0.12%
Mastitis	-6.1	+5.3	1.6	72 + 3 = 75	23%	0.53%
Metritis	-3.3	+2.6	0.9	105 + 7 = 112	20%	0.46%
Retained placenta	-2.4	+1.8	0.8	64 + 4 = 68	11%	0.25%
Health\$	-\$34	+\$16	\$8.5	NA	100%	2.3%
LIV / lactation	-4.1	+3.1	0.6	1,200	NA	7.4%

Conclusions

The inclusion of direct measures of resistance to common health events in genetic selection programs can improve dairy producer profitability. Economic estimates for the cost of health events should reflect the fact that Net Merit already accounts for decreases in production, fertility, and longevity. Emphasis in Net Merit for these six health traits is expected to be approximately 2.3%.

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